

SEQUENCE LISTING

<110> Japan Science and Technology Corporation

<120> A mast cell-specific adapter molecules and cDNAs thereof

<130> 00-F-047PCT/YS

<140> PCT/JP00/06351

<141> 2000-9-17

<150> JP11-263778

<151> 1999-09-17

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 1721

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (255) .. (1562)

<300>

<301> Goitsuka R., et al.

<302> A BASH/SLP-76-related adaptor protein MIST/Clink involved in IgE
receptor-mediated mast cell degranulation

<303> Int. Immunol.

<304> 12

<305> 4

<306> 573-580

<307> 2000

<308> GenBank/AB021220

<309> 2000-05-26

<400> 1

aagaggccaa actgccagg tctgtgctg cgtttctcg aaaacaaaa ctcaacaggc 60
acatacaagg cactctctgc tgaaggactc tctgagggg agagaacatg tcaactctat 120
cttacagagt gctccaggat gcgaccgtg accccctttc caggagctag ccgtctcaac 180
actgagccct tgactaaagg aagactgagc aggctgagtt gaagatccct ctcctttgcc 240
aggtgccaaag gacc atg acc agc cag ggc aat aaa agg aca acg aaa gaa 290
Met Thr Ser Gln Gly Asn Lys Arg Thr Thr Lys Glu
1 5 10
gga ttc ggt gat ctg aga ttc cag aac gtc tct ctg ctg aaa aat agg 338
Gly Phe Gly Asp Leu Arg Phe Gln Asn Val Ser Leu Leu Lys Asn Arg
15 20 25
tca tgg cca agc ctc agc agt gcc aaa ggg cgg tgt cga gcg gtt ctg 386
Ser Trp Pro Ser Leu Ser Ser Ala Lys Gly Arg Cys Arg Ala Val Leu
30 35 40
gaa cca ctt ccg gat cac aga agg aac ttg gct ggg gtc cca ggt gga 434
Glu Pro Leu Pro Asp His Arg Arg Asn Leu Ala Gly Val Pro Gly Gly
45 50 55 60
gaa aaa tgc aac agt aac aac gac tac gaa gat cct gag ttc cag ctg 482
Glu Lys Cys Asn Ser Asn Asn Asp Tyr Glu Asp Pro Glu Phe Gln Leu
65 70 75
ctg aag gca tgg cca tca atg aaa att tta cca gcc aga cct atc cag 530

Leu	Lys	Ala	Trp	Pro	Ser	Met	Lys	Ile	Leu	Pro	Ala	Arg	Pro	Ile	Gln	
			80					85					90			
gaa	tcg	gaa	tac	gca	gat	aca	cgc	tat	ttc	cag	gat	atg	atg	gag	gct	578
Glu	Ser	Glu	Tyr	Ala	Asp	Thr	Arg	Tyr	Phe	Gln	Asp	Met	Met	Glu	Ala	
		95					100				105					
ccc	ctt	ctg	tta	cct	ccc	aag	gct	tct	gtc	tcc	act	gag	aga	caa	acc	626
Pro	Leu	Leu	Leu	Pro	Pro	Lys	Ala	Ser	Val	Ser	Thr	Glu	Arg	Gln	Thr	
	110					115					120					
agg	gat	gtg	agg	atg	aca	cag	ctg	gaa	gaa	gtg	gac	aag	cct	acc	ttc	674
Arg	Asp	Val	Arg	Met	Thr	Gln	Leu	Glu	Glu	Val	Asp	Lys	Pro	Thr	Phe	
125				130						135				140		
aag	gat	gtc	aga	agc	caa	cgc	ttt	aaa	gga	ttc	aaa	tac	aca	aaa	ata	722
Lys	Asp	Val	Arg	Ser	Gln	Arg	Phe	Lys	Gly	Phe	Lys	Tyr	Thr	Lys	Ile	
			145					150					155			
aac	aag	act	cct	ttg	cca	cct	cct	cgg	cct	gct	atc	act	ctc	ccc	aag	770
Asn	Lys	Thr	Pro	Leu	Pro	Pro	Pro	Arg	Pro	Ala	Ile	Thr	Leu	Pro	Lys	
		160						165					170			
aag	tac	caa	ccc	tta	ccc	cca	gca	cca	cca	gag	gag	agc	agt	gca	tac	818
Lys	Tyr	Gln	Pro	Leu	Pro	Pro	Ala	Pro	Pro	Glu	Glu	Ser	Ser	Ala	Tyr	
	175						180					185				
ttc	gct	cca	aag	ccc	acc	ttt	cca	gaa	gtc	cag	agg	ggg	ccc	agg	cag	866
Phe	Ala	Pro	Lys	Pro	Thr	Phe	Pro	Glu	Val	Gln	Arg	Gly	Pro	Arg	Gln	
	190					195					200					
agg	agt	gca	aaa	gac	ttc	agt	agg	gtc	ctt	gga	gca	gaa	gaa	gaa	tct	914
Arg	Ser	Ala	Lys	Asp	Phe	Ser	Arg	Val	Leu	Gly	Ala	Glu	Glu	Glu	Ser	
205					210						215			220		
cac	cac	cag	aca	aag	cca	gaa	tct	tct	tgc	cca	tca	tca	aac	caa	aac	962
His	His	Gln	Thr	Lys	Pro	Glu	Ser	Ser	Cys	Pro	Ser	Ser	Asn	Gln	Asn	

225 230 235
 ada cag aag agt cca cct gcc att gcc agc tct tcc tac atg cca gga 1010
 Thr Gln Lys Ser Pro Pro Ala Ile Ala Ser Ser Ser Tyr Met Pro Gly
 240 245 250
 aag cac agt ata caa gcc aga gac cat aca ggt agc atg cag cac tgt 1058
 Lys His Ser Ile Gln Ala Arg Asp His Thr Gly Ser Met Gln His Cys
 255 260 265
 cct gct cag aga tgc caa gct gca gcc agc cac agc cct cga atg ctg 1106
 Pro Ala Gln Arg Cys Gln Ala Ala Ala Ser His Ser Pro Arg Met Leu
 270 275 280
 ccc tat gaa aac aca aac tgc gag aaa cct gac ccc aca aag cct gat 1154
 Pro Tyr Glu Asn Thr Asn Ser Glu Lys Pro Asp Pro Thr Lys Pro Asp
 285 290 295 300
 gag aag gat gtc tgg cag aat gaa tgg tac att gga gaa tac agt cgc 1202
 Glu Lys Asp Val Trp Gln Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg
 305 310 315
 cag gca gtg gaa gat gtg tta atg aaa gag aac aag gat ggt act ttt 1250
 Gln Ala Val Glu Asp Val Leu Met Lys Glu Asn Lys Asp Gly Thr Phe
 320 325 330
 ttg gtc cga gac tgc tct aca aaa tcc aag gca gaa cca tat gtt ttg 1298
 Leu Val Arg Asp Cys Ser Thr Lys Ser Lys Ala Glu Pro Tyr Val Leu
 335 340 345
 gtg gtg ttt tat ggg aac aag gtc tac aat gtg aaa atc cgt ttc ctc 1346
 Val Val Phe Tyr Gly Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu
 350 355 360
 gag agc aat caa cag ttt gcc ctg ggc aca gga cta cga gga aat gag 1394
 Glu Ser Asn Gln Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asn Glu
 365 370 375 380

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

5 / 13

```

atg ttt gat tct gtg gaa gac atc att gaa cac tac aca tat ttt ccc 1442
Met Phe Asp Ser Val Glu Asp Ile Ile Glu His Tyr Thr Tyr Phe Pro
      385                      390                      395

att ctg cta ata gat ggg aaa gac aag gct gca cgc agg aaa cag tgc 1490
Ile Leu Leu Ile Asp Gly Lys Asp Lys Ala Ala Arg Arg Lys Gln Cys
      400                      405                      410

tac ctc acc cag cca ctg cct ctc gcc agg ctc ctt ctc act cag tac 1538
Tyr Leu Thr Gln Pro Leu Pro Leu Ala Arg Leu Leu Leu Thr Gln Tyr
      415                      420                      425

tcc agc cag gca ctt cat gag taa gaagcccagc cagatatccc cgcatcagtg 1592
Ser Ser Gln Ala Leu His Glu
      430                      435

gcctgggcct tgtctcattc ctggctcaat ggattcagtt cttcttccat ctgcatttat 1652
ctgcaaagta ttattttctg tgtcttcaag ggatgatttt ttgactctgt aaaaaaaaaa 1712
aaaaaaaaaa 1721

```

<210> 2

<211> 435

<212> PRT

<213> Mus musculus

<400> 2

Met Thr Ser Gln Gly Asn Lys Arg Thr Thr Lys Glu Gly Phe Gly Asp
1 5 10 15
Leu Arg Phe Gln Asn Val Ser Leu Leu Lys Asn Arg Ser Trp Pro Ser
20 25 30
Leu Ser Ser Ala Lys Gly Arg Cys Arg Ala Val Leu Glu Pro Leu Pro
35 40 45

THE

Asp	His	Arg	Arg	Asn	Leu	Ala	Gly	Val	Pro	Gly	Gly	Glu	Lys	Cys	Asn
50						55						60			
Ser	Asn	Asn	Asp	Tyr	Glu	Asp	Pro	Glu	Phe	Gln	Leu	Leu	Lys	Ala	Trp
65					70					75					80
Pro	Ser	Met	Lys	Ile	Leu	Pro	Ala	Arg	Pro	Ile	Gln	Glu	Ser	Glu	Tyr
				85					90					95	
Ala	Asp	Thr	Arg	Tyr	Phe	Gln	Asp	Met	Met	Glu	Ala	Pro	Leu	Leu	Leu
				100					105					110	
Pro	Pro	Lys	Ala	Ser	Val	Ser	Thr	Glu	Arg	Gln	Thr	Arg	Asp	Val	Arg
		115						120					125		
Met	Thr	Gln	Leu	Glu	Glu	Val	Asp	Lys	Pro	Thr	Phe	Lys	Asp	Val	Arg
	130					135						140			
Ser	Gln	Arg	Phe	Lys	Gly	Phe	Lys	Tyr	Thr	Lys	Ile	Asn	Lys	Thr	Pro
145					150						155				160
Leu	Pro	Pro	Pro	Arg	Pro	Ala	Ile	Thr	Leu	Pro	Lys	Lys	Tyr	Gln	Pro
				165					170					175	
Leu	Pro	Pro	Ala	Pro	Pro	Glu	Glu	Ser	Ser	Ala	Tyr	Phe	Ala	Pro	Lys
			180					185					190		
Pro	Thr	Phe	Pro	Glu	Val	Gln	Arg	Gly	Pro	Arg	Gln	Arg	Ser	Ala	Lys
		195						200					205		
Asp	Phe	Ser	Arg	Val	Leu	Gly	Ala	Glu	Glu	Glu	Ser	His	His	Gln	Thr
	210					215						220			
Lys	Pro	Glu	Ser	Ser	Cys	Pro	Ser	Ser	Asn	Gln	Asn	Thr	Gln	Lys	Ser
225					230						235				240
Pro	Pro	Ala	Ile	Ala	Ser	Ser	Ser	Tyr	Met	Pro	Gly	Lys	His	Ser	Ile
				245					250					255	
Gln	Ala	Arg	Asp	His	Thr	Gly	Ser	Met	Gln	His	Cys	Pro	Ala	Gln	Arg
				260					265					270	

7/13

Cys Gln Ala Ala Ala Ser His Ser Pro Arg Met Leu Pro Tyr Glu Asn
275 280 285
Thr Asn Ser Glu Lys Pro Asp Pro Thr Lys Pro Asp Glu Lys Asp Val
290 295 300
Trp Gln Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu
305 310 315 320
Asp Val Leu Met Lys Glu Asn Lys Asp Gly Thr Phe Leu Val Arg Asp
325 330 335
Cys Ser Thr Lys Ser Lys Ala Glu Pro Tyr Val Leu Val Val Phe Tyr
340 345 350
Gly Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Ser Asn Gln
355 360 365
Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asn Glu Met Phe Asp Ser
370 375 380
Val Glu Asp Ile Ile Glu His Tyr Thr Tyr Phe Pro Ile Leu Leu Ile
385 390 395 400
Asp Gly Lys Asp Lys Ala Ala Arg Arg Lys Gln Cys Tyr Leu Thr Gln
405 410 415
Pro Leu Pro Leu Ala Arg Leu Leu Leu Thr Gln Tyr Ser Ser Gln Ala
420 425 430
Leu His Glu
435

<210> 3

<211> 1129

<212> DNA

<213> Homo sapiens

8/13

<220>

<221> CDS

<222> (1).. (1128)

<300>

<301> Goitsuka R., et al.

<302> A BASH/SLP-76-related adaptor protein MIST/Clink involved in IgE
receptor-mediated mast cell degranulation

<303> Int. Immunol.

<304> 12

<305> 4

<306> 573-580

<307> 2000

<308> GenBank/AB021220

<309> 2000-05-26

<400> 3

ttc cag aac ttc agt ctg cca aaa aac agg tca tgg cct cgc atc aat 48

Phe Gln Asn Phe Ser Leu Pro Lys Asn Arg Ser Trp Pro Arg Ile Asn

1 5 10 15

agt gcc aca ggc cag tac cag agg atg aac aag cct ctt cta gac tgg 96

Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu Asp Trp

20 25 30

gaa aga aac ttt gct gca gtc ctg gat gga gca aaa ggc cac agt gat 144

Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His Ser Asp

35 40 45

gat gac tat gat gac cct gag ctt cgg atg gaa gag aca tgg cag tgg 192

Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp Gln Ser

50 55 60

THE UNIVERSITY OF CHICAGO

att aaa att tta cca gcc cgg cct ata aag gaa tct gaa tat gca gat	240
Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr Ala Asp	
65 70 75 80	
aca cac tat ttc aag gtt gca atg gac act ccc ctt ccg tta gac acc	288
Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu Asp Thr	
85 90 95	
agg acc tct atc tcc att gga cag ccg acc tgg aac aca cag acg agg	336
Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln Thr Arg	
100 105 110	
ttg gaa aga gtg gac aaa ccc att tcc agg gac gtc aga agc caa aac	384
Leu Glu Arg Val Asp Lys Pro Ile Ser Arg Asp Val Arg Ser Gln Asn	
115 120 125	
att aaa gga gat gca tcc gta aga aag aac aag att cct tta cca cct	432
Ile Lys Gly Asp Ala Ser Val Arg Lys Asn Lys Ile Pro Leu Pro Pro	
130 135 140	
cct cgg cct ctc ata aca ctt ccg aag aag tac caa ccc ttg ccc cct	480
Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu Pro Pro	
145 150 155 160	
gag ccg gag agc agc agg cca cct tta tct cag aga cac acc ttt cca	528
Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr Phe Pro	
165 170 175	
gaa gtc cag gga atg ccc agt cag ata agc tta agg gac tta agt gag	576
Glu Val Gln Gly Met Pro Ser Gln Ile Ser Leu Arg Asp Leu Ser Glu	
180 185 190	
gtc ctt gaa gca gaa aaa gtt cct cat aac cag agg aag cct gaa tca	624
Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro Glu Ser	
195 200 205	
act cat ctg tta gaa aac caa aat act caa gag att cca ctt gcc att	672

220

720

235

240

768

250

255

816

265

270

864

280

285

912

295

300

960

310

315

320

1008

330

335

1056

345

350

1104

Ala Leu Gly Thr/Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser Val Glu

360

1129

Asp Ile Ile Glu His Tyr Lys Asn

375

<400> 4

Phe Gln Asn Phe Ser Leu Pro Lys Asn Arg Ser Trp Pro Arg Ile Asn

5

10

15

Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu Asp Trp

20

25

30

Glu Arg Asn Phe Ala Ala Val / Leu Asp Gly Ala Lys Gly His Ser Asp

35

40

45

Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp Gln Ser

50

55

60

Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr Ala Asp

65

70

75

80

Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu Asp Thr

85

90

95

Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln Thr Arg

100

105

110

Leu Glu Arg Val Asp Lys Pro Ile Ser Arg Asp Val Arg Ser Gln Asn

115

120

125

Ile Lys Gly Asp Ala Ser Val Arg Lys Asn Lys Ile Pro Leu Pro Pro

130 135 140
 Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu Pro Pro
 145 150 155 160
 Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr Phe Pro
 165 170 175
 Glu Val Gln Gly Met Pro Ser Gln Ile Ser Leu Arg Asp Leu Ser Glu
 180 185 190
 Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro Glu Ser
 195 200 205
 Thr His Leu Leu Glu Asn Gln Asn Thr Gln Glu Ile Pro Leu Ala Ile
 210 215 220
 Ser Ser Ser Ser Phe Thr Thr Ser Asn His Ser Val Gln Asn Arg Asp
 225 230 235 240
 His Arg Gly Gly Met Gln Pro Cys Ser Pro Gln Arg Cys Gln Pro Pro
 245 250 255
 Ala Ser Cys Ser Pro His Glu Asn Ile Leu Pro Tyr Lys Tyr Thr Ser
 260 265 270
 Trp Arg Pro Pro Phe Pro Lys Arg Ser Asp Arg Lys Asp Val Gln His
 275 280 285
 Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu Glu Ala
 290 295 300
 Phe Met Lys Glu Asn Lys Asp Gly Ser Phe Leu Val Arg Asp Cys Ser
 305 310 315 320
 Thr Lys Ser Lys Glu Glu Pro Tyr Val Leu Ala Val Phe Tyr Glu Asn
 325 330 335
 Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Arg Asn Gln Gln Phe
 340 345 350
 Ala Leu Gly Thr Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser Val Glu

130 135 140
 145 150 155 160
 165 170 175
 180 185 190
 195 200 205
 210 215 220
 225 230 235 240
 245 250 255
 260 265 270
 275 280 285
 290 295 300
 305 310 315 320
 325 330 335
 340 345 350

375

[illegible]